Appln No.: 09/934,323   Page 1 of 4
Applicant(s): Rory A. J. Curtis
33410, A NOVEL HUMAN CARBOXYLESTERASE FAMILY
MEMBER AND USES THEREOF

1/4

Human 33410

Carboxylesterase Domain
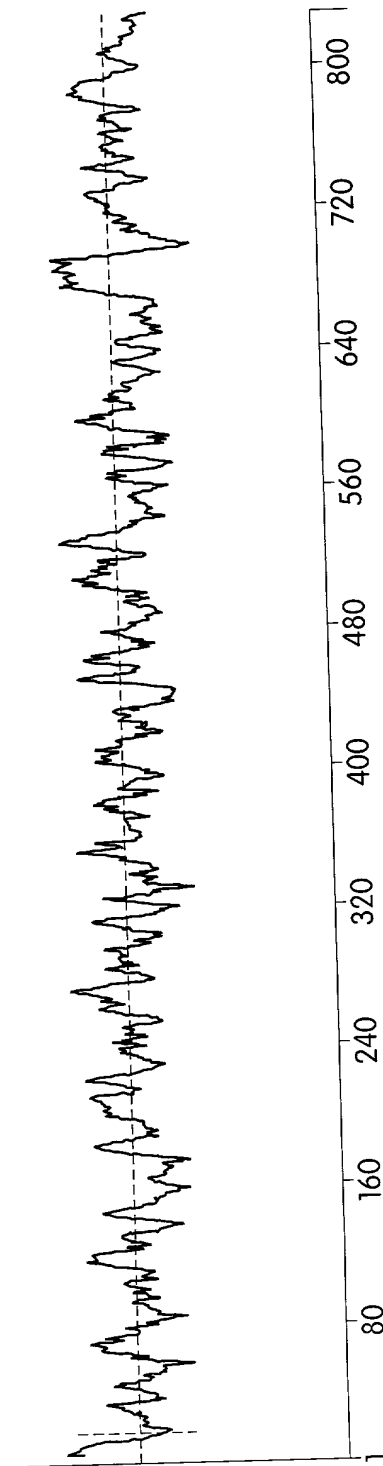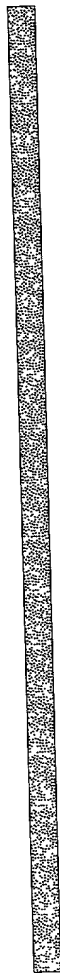

Fig. 1

2/4

```
COesterase: domain 1 of 1, from 42 to 601: score 440.0, E = 2.1e-128
                    *->llVatnnVlcGkvrGvnektdn...geqsvysFlGIPYAePPVGnLR
                       ++V+t +   G vrGv++ ++n+  g  +v  FlG+PYA PP+G  R
    Fbh33410FL      42    PVVNTAY---GRVRGVRRELNNeilG--PVVQFLGVPYATPPLGARR  83


                    FkaPqPYkepWsdvldAtkyppsClQdddfgfslsdLKva.lkmlslgwn
                    F +P+ +   W +v++At+ pp+C+Q+   g      +++ +ml+ ++
    Fbh33410FL      84 FQPPEA-PASWPGVRNATTLPPACPQNLH-G-------ALpAIMLPVWFT 124


                    klvg......lklsEDCLYLNVytPkntkpns.................
                    ++   +    +sEDCLYLN y+P + p  +++++ + ++++++ +++
    Fbh33410FL     125 DNLEaaatyvQNQSEDCLYLNLYVPTEDGPLTkkrdeatlnppdtdirdp 174


                    .klPVmVwIhGGGFmfGsghslplslYdgeslaregnVIvVsiNYRLGpl
                    +k PVm + hGG +m G+g     + dg+ la+ gnVIv ++NYRLG+l
    Fbh33410FL     175 gKKPVMLFLHGGSYMEGTG-----NMFDGSVLAAYGNVIVATLNYRLGVL 219


                    GFLstgddklpgsGNyGLlDQrlALkWVqdNIaaFGGDPnsVTifGeSAG
                    GFLstgd +    GNyGLlDQ+ AL+W +NIa+FGGDP+++TifG AG
    Fbh33410FL     220 GFLSTGDQAAK--GNYGLLDQIQALRWLSENIAHFGGDPERITIFGSGAG 267


                    aaSVslllllsngGDNppsskgLFhRAIsqSGsalspwaiqsesnargrak
                    a+ V 1l+1s       +s+gLF++AI qSG+a+s w++      + ++
    Fbh33410FL     268 ASCVNLLILS------HHSEGLFQKAIAQSGTAISSWSVNYQP--LKYTR 309


                    elarllGCnetssselldCLRsksaeeLleatrsfllfeyvpflplflaF
                    la+++GC++++s+e ++CLR+k+++eL++     ++++y + +
    Fbh33410FL     310 LLAAKVGCDREDSAEAVECLRRKPSRELVDQDV--QPARYHIAFG----- 352


                    gPvvDGdDapeafipedPeelikeGkfadvPyliGvtkdEGgyfaamlln
                    PvvDGd       ++p+dPe+l  +G f + ++liGv++ EG+ f      +
    Fbh33410FL     353 -PVVDGD-----VVPDDPEILMQQGEFLNYDMLIGVNQGEGLKFV----E 392


                    asskgedelkketnpdvwlellkyllfyasealnikdMddladkvlekYp
                    +s+ +ed ++ +++    + ++ l++ +e +    d l ++++ Y+
    Fbh33410FL     393 DSAESEDGVSASAFDF-TVSNFVDNLYGYPEGK-----DVLRETIKFMYT 436


                    gdvddfsvesrkpnlqdmltDllFkcptrvaadlhakhggsPvYaYvfdh
                    +++d+   e r++ l+ ++tD+ + p +va ++ +++ +sPvY+Y f h
    Fbh33410FL     437 DWADRDNGEMRRKTLLALFTDHQWVAP-AVATAKLHADYQSPVYFYTFYH 485


                    pasfgigQflakrvdpefggavHgdEiffvFgnpllkeqlyka...teee
                    + +       +pe+  a HgdE+++vFg+p + ++ + + ++ +
    Fbh33410FL     486 HCQ--------AEGRPEWADAAHGDELPYVFGVPMVGATDLFPcnfSKND 527


                    eksssktmmnywanFAktGnPn....ngts........nglvvWpkytse
                    +++s ++m yw+nFAktG+Pn++ + +t   +++++++++vvW k++s+
    Fbh33410FL     528 VMLS-AVVMTYWTNFAKTGDPNqpvpQDTKfihtkpnrFEEVVWSKFNSK 576


                    eqkYsllillttitaqklkardprkvlcnfw<-*
                    e +l+i l+  ++++a++     ++fw
    Fbh33410FL     577 EKQ-YLHIGLKPRVRDNYRANK-----VAFW        601
```

Fig. 2

3/4

CLUSTAL W (1.74) multiple sequence alignment

```
Fbh33410FL    MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVRGVRRELNN
ratNL2 =      MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVRGVRRELNN
              ************************************************************


Fbh33410FL    EILGPVVQFLGVPYATPPLGARRFQPPEAPASWPGVRNATTLPPACPQNLHGALPAIMLP
ratNL2        EILGPVVQFLGVPYATPPLGARRFQPPEAPASWPGVRNATTLPPACPQNLHGALPAIMLP
              ************************************************************


Fbh33410FL    VWFTDNLEAAATYVQNQSEDCLYLNLYVPTEDGPLTKKRDEATLNPPDTDIRDPGKKPVM
ratNL2        VWFTDNLEAAATYVQNQSEDCLYLNLYVPTEDGPLTKKRDEATLNPPDTDIRDSGKKPVM
              *****************************************************.******


Fbh33410FL    LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNYRLGVLGFLSTGDQAAKGNYGLLDQIQ
ratNL2        LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNYRLGVLGFLSTGDQAAKGNYGLLDQIQ
              ************************************************************


Fbh33410FL    ALRWLSENIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIAQSGTAISSWSV
ratNL2        ALRWLSENIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIAQSGTAISSWSV
              ************************************************************


Fbh33410FL    NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
ratNL2        NYQPLKYTRLLAAKVGCDREDSTEAVECLRRKSSRELVDQDVQPARYHIAFGPVVDGDVV
              **********************:********.*****************************


Fbh33410FL    PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
ratNL2        PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
              ************************************************************


Fbh33410FL    PEGKDVLRETIKFMYTDWADRDNGEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF
ratNL2        PEGKDVLRETIKFMYTDWADRDNGEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF
              ************************************************************


Fbh33410FL    YTFYHHCQAEGRPEWADAAHGDELPYVFGVPMVGATDLFPCNFSKNDVMLSAVVMTYWTN
ratNL2        YTFYHHCQAEGRPEWADAAHGDELPYVFGVPMVGATDLFPCNFSKNDVMLSAVVMTYWTN
              ************************************************************


Fbh33410FL    FAKTGDPNQPVPQDTKFIHTKPNRPEEVVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
ratNL2        FAKTGDPNQPVPQDTKFIHTKPNRFEEVVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
              ************************************************************


Fbh33410FL    WLELVPHLHNLHTELFTTTTRLPPYATRWPPRPP-AGAPGTRRPPPPATLPPEPEPEPGP
ratNL2        WLELVPHLHNLHTELFTTTTRLPPYATRWPPRTPGPGTSGTRRPPPPATLPPESDIDLGP
              ********************************.*  .*:.**************.: : **
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```
                                   TM1
Fbh33410FL    RAYDRFPGDSRDYSTELSVTVAVGASLLFLNILAFAALYYKRDRRQELRCRRLSPPGGSG
ratNL2        RAYDRFPGDSRDYSTELSVTVAVGASLLFLNILAFAALYYKRDRRQELRCRRLSPPGGSG
              ***************|**************************|******************
```

```
Fbh33410FL    SGVPGGGPLLPAAGRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDD
ratNL2        SGVPGGGPLLPTAGRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDD
              ***********.************************************************


Fbh33410FL    VPLLAPGALTLLPSGLGPPPPPPPPPSLHPFGPFPPPPPPTATSHNNTLPHPHSTTRV
ratNL2        VPLLAPGALTLLPSGLGPPPPPPPPPSLHPFGPFPPPPPPTATSHNNTLPHPHSTTRV
              **********************************************************
```

Fig. 3

4/4

CLUSTAL W (1.74) multiple sequence alignment

```
Fbh33410FL    MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVRGVRRELNN
KIAA1366      ------------------------------------------------------------


Fbh33410FL    EILGPVVQFLGVPYATPPLGARRFQPPEAPASWPGVRNATTLPPACPQNLHGALPAIMLP
KIAA1366      ------------------------------------------------------------


Fbh33410FL    VWFTDNLEAAATYVQNQSEDCLYLNLYVPTEDGPLTKKRDEATLNPPDTDIRDPGKKPVM
KIAA1366      ------------------------------------------------------------


Fbh33410FL    LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNYRLGVLGFLSTGDQAAKGNYGLLDQIQ
KIAA1366      ------------------------------------------------------------


Fbh33410FL    ALRWLSENIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIAQSGTAISSWSV
KIAA1366      ---------------------------------------------KAIAQSGTAISSWSV
                                                           ***************


Fbh33410FL    NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
KIAA1366      NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
              ************************************************************


Fbh33410FL    PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
KIAA1366      PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
              ************************************************************


Fbh33410FL    PEGKDVLRETIKFMYTDWADRDNGEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF
KIAA1366      PEGKDVLRETIKFMYTDWADRDNGEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF
              ************************************************************


Fbh33410FL    YTFYHHCQAEGRPEWADAAHGDELPYVFGVPMVGATDLFPCNFSKNDVMLSAVVMTYWTN
KIAA1366      YTFYHHCQAEGRPEWADAAHGDELPYVFGVPMVGATDLFPCNFSKNDVMLSAVVMTYWTN
              ************************************************************


Fbh33410FL    FAKTGDPNQPVPQDTKFIHTKPNRFEEVVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
KIAA1366      FAKTGDPNQPVPQDTKFIHTKPNRFEEVVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
              ************************************************************


Fbh33410FL    WLELVPHLHNLHTELFTTTTRLPPYATRWPPRPPAGAPGTRRPPPPATLPPEPEPEPGPR
KIAA1366      WLELVPHLHNLHTELFTTTTRLPPYATRWPPRPPAGAPGTRRPPPPATLPPEPEPEPGPR
              ************************************************************


Fbh33410FL    AYDRFPGDSRDYSTELSVTVAVGASLLFLNILAFAALYYKRDRRQELRCRRLSPPGGSGS
KIAA1366      AYDRFPGDSRDYSTELSVTVAVGASLLFLNILAFAALYYKRDRRQELRCRRLSPPGGSGS
              ************************************************************


Fbh33410FL    GVPGGGPLLPAAGRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDDV
KIAA1366      GVPGGGPLLPAAGRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDDV
              ************************************************************


Fbh33410FL    PLLAPGALTLLPSGLGPPPPPPPPSLHPFGPFPPPPPTATSHNNTLPHPHSTTRV
KIAA1366      PLLAPGALTLLPSGLGPPPPPPPPSLHPFGPFPPPPPTATSHNNTLPHPHSTTRV
              ******************************************************
```

Fig. 4